

SEQUENCE LISTING

<110> GROSS, RICHARD W.
DAVID J. MANCUSO

<120> CALCIUM INDEPENDENT PHOSPHOLIPASE A2 γ POLYNUCLEOTIDES
AND POLYPEPTIDES AND METHODS THEREFOR

<130> 15060-58

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<150> 09/168,623

<151> 2000-07-18

<160> 104

<170> PatentIn Ver. 3.2

<210> 1

<211> 782

<212> PRT

<213> Homo sapiens

<400> 1

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Gly	Phe	His	Thr	Asn	Ile	Ile	Arg	Cys	Lys	Trp	Thr	Lys	Ser	Glu	Ala	50	55	60	
His	Ser	Cys	Ser	Lys	His	Cys	Tyr	Ser	Pro	Ser	Asn	His	Gly	Leu	His	65	70	75	80
Ile	Gly	Ile	Leu	Lys	Leu	Ser	Thr	Ser	Ala	Pro	Lys	Gly	Leu	Thr	Lys	85	90	95	
Val	Asn	Ile	Cys	Met	Ser	Arg	Ile	Lys	Ser	Thr	Leu	Asn	Ser	Val	Ser	100	105	110	
Lys	Ala	Val	Phe	Gly	Asn	Gln	Asn	Glu	Met	Ile	Ser	Arg	Leu	Ala	Gln	115	120	125	
Phe	Lys	Pro	Ser	Ser	Gln	Ile	Leu	Arg	Lys	Val	Ser	Asp	Ser	Gly	Trp	130	135	140	
Leu	Lys	Gln	Lys	Asn	Ile	Lys	Gln	Ala	Ile	Lys	Ser	Leu	Lys	Lys	Tyr	145	150	155	160

Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His
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 Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr
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 Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser
 195 200 205
 Asn His Ile Asn Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln
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 Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys
 225 230 235 240
 Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr
 245 250 255
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 260 265 270
 Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala
 275 280 285
 Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly
 290 295 300
 Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln
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 Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys
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 Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys
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 Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu
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 Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala
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 405 410 415
 Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly
 420 425 430
 Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp
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 Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu
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Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys
 465 470 475 480
 Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His
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 Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp
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 Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser
 515 520 525
 His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg
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 Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro
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 Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys
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 Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser
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 His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met
 625 630 635 640
 His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val
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 Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr
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 Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr
 675 680 685
 Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp
 690 695 700
 Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp
 705 710 715 720
 Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys
 725 730 735
 Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu
 740 745 750
 Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu
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 atgattacct gaagtttaaat aagtaagacc atgaattatg gcatttctta aatgaagcgt 180
 tcaagaagtg agagaatgtc atagaaaata aatgatTTTT aagttatgtc tattaatctg 240
 actgtagata tatatatTTA cctccttagt aatgcaagaa gtgtttgtgg gaagcagaga 300
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 nttaaatgaa gcgttcaaga agtgagagaa tgtcatanaa aataaatgat ttttaagtta 180
 tgtctattaa tctgactgta gatatatata ttacctcct tagtaatgca agaagtgttt 240

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Arg Ala Ser Arg Arg Cys Ser Pro Ser Asp Cys Gly Leu His Pro Asp
15 20 25
tgt ctt ctc ctc caa ggt cta cat gat tac ctg aag ttt aat aat aat 146
Cys Leu Leu Leu Gln Gly Leu His Asp Tyr Leu Lys Phe Asn Asn Asn
30 35 40
gca aga agt gtt tgt ggg aag cag aga agc aag caa ctg tat ttc tt 193
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atgattacct gaagtttaat aagtaagacc atgaattatg gcattttctta aatgaagcgt 180
tcaagaagtg agagaatgtc atagaaaata aatgattttt aagtt atg tct att aat 237
Met Ser Ile Asn
1
ctg act gta gat ata tat att tac ctc ctt agt aat gca aga agt gtt 285
Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn Ala Arg Ser Val
5 10 15 20
tgt ggg aag cag aga agc aag caa ctg tat ttc ttg ttc tca cct aag 333
Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu Phe Ser Pro Lys
25 30 35

cat tac tgg agg ata agc cac atc agt cta caa aga ggt ttt cat aca 381
 His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg Gly Phe His Thr
 40 45 50

aac ata ata aga tgt aaa tgg acc aaa agt gaa gca cat tct tgc agt 429
 Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala His Ser Cys Ser
 55 60 65

aag cac tgt tac tct cca agc aac cat ggt tta cat att ggg att ttg 477
 Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His Ile Gly Ile Leu
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aaa ctt agc act tct gct ccc aag gga ctt aca aaa gtg aac att tgt 525
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 85 90 95 100

atg tcc cgt att aaa agt act ttg aac tct gtt tca aag gct gtt ttt 573
 Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser Lys Ala Val Phe
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ggc aat caa aat gaa atg att tca cgt tta gct caa ttt aag cca agt 621
 Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser
 120 125 130

tcc caa att tta aga aaa gta tcg gat agt ggc tgg tta aaa cag aaa 669
 Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp Leu Lys Gln Lys
 135 140 145

aac atc aaa caa gcc atc aaa tct ctg aaa aaa tat agt gac aaa tca 717
 Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser
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gca gaa aag agt cct ttt cca gaa gag aaa agt cac att ata gac aaa 765
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 165 170 175 180

gaa gaa gat ata ggt aaa cgc agt ctt ttt cat tac aca agt tct ata 813
 Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile
 185 190 195

acc aca aaa ttt gga gac tca ttc tac ttt tta tca aat cat att aat 861
 Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn
 200 205 210

tca tat ttc aaa cgt aag gaa aaa atg tct caa caa aag gaa aat gaa 909
 Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu
 215 220 225

cat ttc cgg gac aaa tca gaa ctt gaa gat aaa aag gta gaa gag ggg 957
 His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly
 230 235 240

aaa tta aga tct cca gat cct ggc atc ctg gct tat aag cca ggc tca 1005
 Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser
 245 250 255 260

gaa tct gta cat acg gtg gac aag cct aca agt cct tct gcg ata cct	1053
Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro	
265 270 275	
gat gtt ctt caa gtt tca act aaa caa agt att gct aac ttt ctt tct	1101
Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser	
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Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly	
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Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln	
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gaa gag cct gct aaa act gat cag gct gtc agc aaa gac aga aat gca	1245
Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala	
325 330 335 340	
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Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg	
345 350 355	
gtg agt att gat aac agg acc cgg gca tta gtt cag gca tta aga aga	1341
Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg	
360 365 370	
aca act gac cca aag ctc tgc att act agg gtt gaa gaa ctg act ttt	1389
Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe	
375 380 385	
cat ctt cta gaa ttt cct gaa gga aaa gga gtg gct gtc aag gaa aga	1437
His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg	
390 395 400	
att att cca tat tta tta cga ctg aga caa att aag gat gaa act ctt	1485
Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu	
405 410 415 420	
cag gct gca gtt aga gaa att ttg gcc cta att ggc tat gtg gat cca	1533
Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro	
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Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr	
440 445 450	
agg ggc gtg gtt gct ctc cag acc cta cga aaa tta gtt gaa ctt act	1629
Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr	
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Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr	
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ctg atg att gaa aca gca aga aac ccc aca tgt cct aag gta gct gct Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala 550 555 560	1917
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ggt ttg ctt ctg aat aac cct tcg gca tta gct atg cat gag tgt aaa Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys 630 635 640	2157
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gtc cat ata atg ctt gat ggc ctg tta cct cct gac acc tat ttt aga Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg 695 700 705	2349


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gaa aag ctg gat cag ctg cag ttg gaa ggg ttg aaa tac ata gaa aga 2445
Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg
    725                      730                      735                      740

aat gaa caa aaa atg aaa aaa gtt gca aaa ata tta agt caa gaa aaa 2493
Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys
    745                      750                      755

aca act ctg cag aaa att aat gat tgg ata aaa tta aaa act gat atg 2541
Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met
    760                      765                      770

tat gaa gga ctt cca ttc ttt tca aaa ttg tgatgagtat atgcttatgt 2591
Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu
    775                      780

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gacatgagtt aactttgaaa tacgtatgaa ttctggagaa tcctgaaaaa gacgggtgctt 2711
caaccagctt gcatagcaca gagaatattc ttggttacag aattcatatg ggaactaggc 2771
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gacatttctct cacttcttga acgcttcatt taanaaatgc cataattcat ggtcttaccg 180
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gggctgcagc ggcgactcgc tcgttcccgg caatgacgtc cactccaacc ggctgcatc 180
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38

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Ala	Arg	Ser	Val	Cys	Gly	Lys	Gln	Arg	Ser	Lys	Gln	Leu	Tyr	Phe	Leu	
			20				25					30				

ttc	tca	cct	aag	cat	tac	tgg	agg	ata	agc	cac	atc	agt	cta	caa	aga	144
Phe	Ser	Pro	Lys	His	Tyr	Trp	Arg	Ile	Ser	His	Ile	Ser	Leu	Gln	Arg	
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ggt	ttt	cat	aca	aac	ata	ata	aga	tgt	aaa	tgg	acc	aaa	agt	gaa	gca	192
Gly	Phe	His	Thr	Asn	Ile	Ile	Arg	Cys	Lys	Trp	Thr	Lys	Ser	Glu	Ala	
	50				55				60							

cat	tct	tgc	agt	aag	cac	tgt	tac	tct	cca	agc	aac	cat	ggt	tta	cat	240
His	Ser	Cys	Ser	Lys	His	Cys	Tyr	Ser	Pro	Ser	Asn	His	Gly	Leu	His	
	65				70				75				80			

att	ggg	att	ttg	aaa	ctt	agc	act	tct	gct	ccc	aag	gga	ctt	aca	aaa	288
Ile	Gly	Ile	Leu	Lys	Leu	Ser	Thr	Ser	Ala	Pro	Lys	Gly	Leu	Thr	Lys	
			85					90					95			

gtg aac att tgt atg tcc cgt att aaa agt act ttg aac tct gtt tca	336
Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser	
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aag gct gtt ttt ggc aat caa aat gaa atg att tca cgt tta gct caa	384
Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln	
115 120 125	
ttt aag cca agt tcc caa att tta aga aaa gta tcg gat agt ggc tgg	432
Phe Lys Pro Ser Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp	
130 135 140	
tta aaa cag aaa aac atc aaa caa gcc atc aaa tct ctg aaa aaa tat	480
Leu Lys Gln Lys Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr	
145 150 155 160	
agt gac aaa tca gca gaa aag agt cct ttt cca gaa gag aaa agt cac	528
Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His	
165 170 175	
att ata gac aaa gaa gaa gat ata ggt aaa cgc agt ctt ttt cat tac	576
Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr	
180 185 190	
aca agt tct ata acc aca aaa ttt gga gac tca ttc tac ttt tta tca	624
Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser	
195 200 205	
aat cat att aat tca tat ttc aaa cgt aag gaa aaa atg tct caa caa	672
Asn His Ile Asn Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln	
210 215 220	
aag gaa aat gaa cat ttc cgg gac aaa tca gaa ctt gaa gat aaa aag	720
Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys	
225 230 235 240	
gta gaa gag ggg aaa tta aga tct cca gat cct ggc atc ctg gct tat	768
Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr	
245 250 255	
aag cca ggc tca gaa tct gta cat acg gtg gac aag cct aca agt cct	816
Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro	
260 265 270	
tct gcg ata cct gat gtt ctt caa gtt tca act aaa caa agt att gct	864
Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala	
275 280 285	
aac ttt ctt tct cgt ccc acg gaa ggt gta caa gct tta gta ggt ggt	912
Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly	
290 295 300	
tat att ggt gga ctt gtc ccc aaa tta aag tat gat tca aag agt cag	960
Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln	
305 310 315 320	

tca gaa gaa cag gaa gag cct gct aaa act gat cag gct gtc agc aaa	1008
Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys	
325 330 335	
gac aga aat gca gag gag aaa aag cgt tta tct ctt cag cga gaa aag	1056
Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys	
340 345 350	
att atc gca agg gtg agt att gat aac agg acc cgg gca tta gtt cag	1104
Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln	
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gca tta aga aga aca act gac cca aag ctc tgc att act agg gtt gaa	1152
Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu	
370 375 380	
gaa ctg act ttt cat ctt cta gaa ttt cct gaa gga aaa gga gtg gct	1200
Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala	
385 390 395 400	
gtc aag gaa aga att att cca tat tta tta cga ctg aga caa att aag	1248
Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys	
405 410 415	
gat gaa act ctt cag gct gca gtt aga gaa att ttg gcc cta att ggc	1296
Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly	
420 425 430	
tat gtg gat cca gtg aaa ggg aga gga atc cga att ctc tca att gat	1344
Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp	
435 440 445	
ggg gga gga aca agg ggc gtg gtt gct ctc cag acc cta cga aaa tta	1392
Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu	
450 455 460	
gtt gaa ctt act cag aag cca gtt cat cag ctc ttt gat tac att tgt	1440
Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys	
465 470 475 480	
ggg gta agc aca ggt gcc ata tta gct ttc atg ttg ggg ttg ttt cat	1488
Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His	
485 490 495	
atg ccc ttg gat gaa tgt gag gaa ctt tat cga aaa tta gga tca gat	1536
Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp	
500 505 510	
gta ttt tca caa aat gtc att gtt gga aca gta aaa atg agt tgg agc	1584
Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser	
515 520 525	
cat gca ttt tat gac agt caa aca tgg gaa aac att ctt aag gat agg	1632
His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg	
530 535 540	

atg gga tct gca ctg atg att gaa aca gca aga aac ccc aca tgt cct	1680
Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro	
545 550 555 560	
aag gta gct gct gta agt acc ata gta aat aga ggg ata aca ccc aaa	1728
Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys	
565 570 575	
gct ttt gtg ttc aga aac tat ggt cat ttt cct gga atc aac tct cat	1776
Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His	
580 585 590	
tat ttg gga ggc tgt cag tat aaa atg tgg cag gcc att aga gcc tca	1824
Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser	
595 600 605	
tct gct gct cca ggc tac ttt gca gaa tat gca ttg gga aat gat ctt	1872
Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu	
610 615 620	
cat caa gat gga ggt ttg ctt ctg aat aac cct tcg gca tta gct atg	1920
His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met	
625 630 635 640	
cat gag tgt aaa tgt ctt tgg cca gat gtg ccg tta gag tgc ata gta	1968
His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val	
645 650 655	
tcc ctg ggc act gga cgt tat gag agt gat gtg aga aac acg gta aca	2016
Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr	
660 665 670	
tac aca agc ttg aaa act aaa ctt tct aat gtt atc aac agt gct aca	2064
Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr	
675 680 685	
gat aca gaa gaa gtc cat ata atg ctt gat ggc ctg tta cct cct gac	2112
Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp	
690 695 700	
acc tat ttt aga ttc aat cct gta atg tgt gaa aac ata cct cta gat	2160
Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp	
705 710 715 720	
gaa agt cga aat gaa aag ctg gat cag ctg cag ttg gaa ggg ttg aaa	2208
Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys	
725 730 735	
tac ata gaa aga aat gaa caa aaa atg aaa aaa gtt gca aaa ata tta	2256
Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu	
740 745 750	
agt caa gaa aaa aca act ctg cag aaa att aat gat tgg ata aaa tta	2304
Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu	
755 760 765	

aaa act gat atg tat gaa gga ctt cca ttc ttt tca aaa ttg tga 2349
 Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu
 770 775 780

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 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 15
 <211> 682
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser
 50 55 60
 Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys
 65 70 75 80
 Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile
 85 90 95
 Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn
 100 105 110
 Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu
 115 120 125
 His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly
 130 135 140
 Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser
 145 150 155 160
 Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro
 165 170 175

Asp	Val	Leu	Gln	Val	Ser	Thr	Lys	Gln	Ser	Ile	Ala	Asn	Phe	Leu	Ser	180	185	190
Arg	Pro	Thr	Glu	Gly	Val	Gln	Ala	Leu	Val	Gly	Gly	Tyr	Ile	Gly	Gly	195	200	205
Leu	Val	Pro	Lys	Leu	Lys	Tyr	Asp	Ser	Lys	Ser	Gln	Ser	Glu	Glu	Gln	210	215	220
Glu	Glu	Pro	Ala	Lys	Thr	Asp	Gln	Ala	Val	Ser	Lys	Asp	Arg	Asn	Ala	225	230	235
Glu	Glu	Lys	Lys	Arg	Leu	Ser	Leu	Gln	Arg	Glu	Lys	Ile	Ile	Ala	Arg	245	250	255
Val	Ser	Ile	Asp	Asn	Arg	Thr	Arg	Ala	Leu	Val	Gln	Ala	Leu	Arg	Arg	260	265	270
Thr	Thr	Asp	Pro	Lys	Leu	Cys	Ile	Thr	Arg	Val	Glu	Glu	Leu	Thr	Phe	275	280	285
His	Leu	Leu	Glu	Phe	Pro	Glu	Gly	Lys	Gly	Val	Ala	Val	Lys	Glu	Arg	290	295	300
Ile	Ile	Pro	Tyr	Leu	Leu	Arg	Leu	Arg	Gln	Ile	Lys	Asp	Glu	Thr	Leu	305	310	315
Gln	Ala	Ala	Val	Arg	Glu	Ile	Leu	Ala	Leu	Ile	Gly	Tyr	Val	Asp	Pro	325	330	335
Val	Lys	Gly	Arg	Gly	Ile	Arg	Ile	Leu	Ser	Ile	Asp	Gly	Gly	Gly	Thr	340	345	350
Arg	Gly	Val	Val	Ala	Leu	Gln	Thr	Leu	Arg	Lys	Leu	Val	Glu	Leu	Thr	355	360	365
Gln	Lys	Pro	Val	His	Gln	Leu	Phe	Asp	Tyr	Ile	Cys	Gly	Val	Ser	Thr	370	375	380
Gly	Ala	Ile	Leu	Ala	Phe	Met	Leu	Gly	Leu	Phe	His	Met	Pro	Leu	Asp	385	390	395
Glu	Cys	Glu	Glu	Leu	Tyr	Arg	Lys	Leu	Gly	Ser	Asp	Val	Phe	Ser	Gln	405	410	415
Asn	Val	Ile	Val	Gly	Thr	Val	Lys	Met	Ser	Trp	Ser	His	Ala	Phe	Tyr	420	425	430
Asp	Ser	Gln	Thr	Trp	Glu	Asn	Ile	Leu	Lys	Asp	Arg	Met	Gly	Ser	Ala	435	440	445
Leu	Met	Ile	Glu	Thr	Ala	Arg	Asn	Pro	Thr	Cys	Pro	Lys	Val	Ala	Ala	450	455	460
Val	Ser	Thr	Ile	Val	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Ala	Phe	Val	Phe	465	470	475
																		480

Arg	Asn	Tyr	Gly	His 485	Phe	Pro	Gly	Ile	Asn 490	Ser	His	Tyr	Leu	Gly 495	Gly
Cys	Gln	Tyr	Lys	Met	Trp	Gln	Ala	Ile 505	Arg	Ala	Ser	Ser	Ala 510	Ala	Pro
Gly	Tyr	Phe	Ala	Glu	Tyr	Ala	Leu 520	Gly	Asn	Asp	Leu	His 525	Gln	Asp	Gly
Gly	Leu 530	Leu	Leu	Asn	Asn	Pro 535	Ser	Ala	Leu	Ala	Met 540	His	Glu	Cys	Lys
Cys 545	Leu	Trp	Pro	Asp	Val 550	Pro	Leu	Glu	Cys	Ile 555	Val	Ser	Leu	Gly	Thr 560
Gly	Arg	Tyr	Glu	Ser 565	Asp	Val	Arg	Asn	Thr 570	Val	Thr	Tyr	Thr	Ser 575	Leu
Lys	Thr	Lys	Leu 580	Ser	Asn	Val	Ile	Asn 585	Ser	Ala	Thr	Asp	Thr 590	Glu	Glu
Val	His 595	Ile	Met	Leu	Asp	Gly	Leu 600	Leu	Pro	Pro	Asp	Thr 605	Tyr	Phe	Arg
Phe	Asn 610	Pro	Val	Met	Cys	Glu 615	Asn	Ile	Pro	Leu	Asp 620	Glu	Ser	Arg	Asn
Glu 625	Lys	Leu	Asp	Gln	Leu 630	Gln	Leu	Glu	Gly	Leu 635	Lys	Tyr	Ile	Glu	Arg 640
Asn	Glu	Gln	Lys	Met 645	Lys	Lys	Val	Ala	Lys 650	Ile	Leu	Ser	Gln	Glu 655	Lys
Thr	Thr	Leu	Gln 660	Lys	Ile	Asn	Asp	Trp 665	Ile	Lys	Leu	Lys	Thr 670	Asp	Met
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<210> 16
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<212> DNA
<213> Homo sapiens
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	1			5					10					15		
ggc	aat	caa	aat	gaa	atg	att	tca	cgt	tta	gct	caa	ttt	aag	cca	agt	96
Gly	Asn	Gln	Asn	Glu	Met	Ile	Ser	Arg	Leu	Ala	Gln	Phe	Lys	Pro	Ser	
			20					25					30			

tcc caa att tta aga aaa gta tcg gat agt ggc tgg tta aaa cag aaa	144
Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp Leu Lys Gln Lys	
35 40 45	
aac atc aaa caa gcc atc aaa tct ctg aaa aaa tat agt gac aaa tca	192
Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser	
50 55 60	
gca gaa aag agt cct ttt cca gaa gag aaa agt cac att ata gac aaa	240
Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys	
65 70 75 80	
gaa gaa gat ata ggt aaa cgc agt ctt ttt cat tac aca agt tct ata	288
Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile	
85 90 95	
acc aca aaa ttt gga gac tca ttc tac ttt tta tca aat cat att aat	336
Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn	
100 105 110	
tca tat ttc aaa cgt aag gaa aaa atg tct caa caa aag gaa aat gaa	384
Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu	
115 120 125	
cat ttc cgg gac aaa tca gaa ctt gaa gat aaa aag gta gaa gag ggg	432
His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly	
130 135 140	
aaa tta aga tct cca gat cct ggc atc ctg gct tat aag cca ggc tca	480
Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser	
145 150 155 160	
gaa tct gta cat acg gtg gac aag cct aca agt cct tct gcg ata cct	528
Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro	
165 170 175	
gat gtt ctt caa gtt tca act aaa caa agt att gct aac ttt ctt tct	576
Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser	
180 185 190	
cgt ccc acg gaa ggt gta caa gct tta gta ggt ggt tat att ggt gga	624
Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly	
195 200 205	
ctt gtc ccc aaa tta aag tat gat tca aag agt cag tca gaa gaa cag	672
Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln	
210 215 220	
gaa gag cct gct aaa act gat cag gct gtc agc aaa gac aga aat gca	720
Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala	
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gag gag aaa aag cgt tta tct ctt cag cga gaa aag att atc gca agg	768
Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg	
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Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg	
260 265 270	
aca act gac cca aag ctc tgc att act agg gtt gaa gaa ctg act ttt	864
Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe	
275 280 285	
cat ctt cta gaa ttt cct gaa gga aaa gga gtg gct gtc aag gaa aga	912
His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg	
290 295 300	
att att cca tat tta tta cga ctg aga caa att aag gat gaa act ctt	960
Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu	
305 310 315 320	
cag gct gca gtt aga gaa att ttg gcc cta att ggc tat gtg gat cca	1008
Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro	
325 330 335	
gtg aaa ggg aga gga atc cga att ctc tca att gat ggt gga gga aca	1056
Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr	
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Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr	
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Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr	
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Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His Met Pro Leu Asp	
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Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln	
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aat gtc att gtt gga aca gta aaa atg agt tgg agc cat gca ttt tat	1296
Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr	
420 425 430	
gac agt caa aca tgg gaa aac att ctt aag gat agg atg gga tct gca	1344
Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala	
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Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala	
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Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe	
465 470 475 480	

aga aac tat ggt cat ttt cct gga atc aac tct cat tat ttg gga ggc	1488
Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly	
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Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly	
515 520 525	
ggc ttg ctt ctg aat aac cct tgc gca tta gct atg cat gag tgt aaa	1632
Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys	
530 535 540	
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Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr	
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Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu	
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Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu	
580 585 590	
gtc cat ata atg ctt gat ggc ctg tta cct cct gac acc tat ttt aga	1824
Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg	
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ttc aat cct gta atg tgt gaa aac ata cct cta gat gaa agt cga aat	1872
Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn	
610 615 620	
gaa aag ctg gat cag ctg cag ttg gaa ggg ttg aaa tac ata gaa aga	1920
Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg	
625 630 635 640	
aat gaa caa aaa atg aaa aaa gtt gca aaa ata tta agt caa gaa aaa	1968
Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys	
645 650 655	
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Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met	
660 665 670	
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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27

<210> 18

<211> 661

<212> PRT

<213> Homo sapiens

<400> 18

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Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser Ala Glu Lys Ser Pro
          35             40             45

Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys Glu Glu Asp Ile Gly
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Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile Thr Thr Lys Phe Gly
          65             70             75             80

Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn Ser Tyr Phe Lys Arg
          85             90             95

Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys
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Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro
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Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr
          130            135            140

Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val
          145            150            155            160

Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly
          165            170            175

Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu
          180            185            190

Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys
          195            200            205

Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg
          210            215            220

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Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn
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 245 250 255
 Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe
 260 265 270
 Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu
 275 280 285
 Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg
 290 295 300
 Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly
 305 310 315 320
 Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala
 325 330 335
 Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His
 340 345 350
 Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala
 355 360 365
 Phe Met Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu
 370 375 380
 Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly
 385 390 395 400
 Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp
 405 410 415
 Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr
 420 425 430
 Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val
 435 440 445
 Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His
 450 455 460
 Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met
 465 470 475 480
 Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu
 485 490 495
 Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn
 500 505 510
 Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp
 515 520 525

Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser
530 535 540

Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser
545 550 555 560

Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu
565 570 575

Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met
580 585 590

Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln
595 600 605

Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met
610 615 620

Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys
625 630 635 640

Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro
645 650 655

Phe Phe Ser Lys Leu
660

<210> 19
<211> 1986
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1983)

<400> 19
atg att tca cgt tta gct caa ttt aag cca agt tcc caa att tta aga 48
Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser Ser Gln Ile Leu Arg
1 5 10 15

aaa gta tcg gat agt ggc tgg tta aaa cag aaa aac atc aaa caa gcc 96
Lys Val Ser Asp Ser Gly Trp Leu Lys Gln Lys Asn Ile Lys Gln Ala
20 25 30

atc aaa tct ctg aaa aaa tat agt gac aaa tca gca gaa aag agt cct 144
Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser Ala Glu Lys Ser Pro
35 40 45

ttt cca gaa gag aaa agt cac att ata gac aaa gaa gaa gat ata ggt 192
Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys Glu Glu Asp Ile Gly
50 55 60

aaa cgc agt ctt ttt cat tac aca agt tct ata acc aca aaa ttt gga 240
Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile Thr Thr Lys Phe Gly
65 70 75 80

gac tca ttc tac ttt tta tca aat cat att aat tca tat ttc aaa cgt	288
Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn Ser Tyr Phe Lys Arg	
85 90 95	
aag gaa aaa atg tct caa caa aag gaa aat gaa cat ttc cgg gac aaa	336
Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys	
100 105 110	
tca gaa ctt gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca	384
Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro	
115 120 125	
gat cct ggc atc ctg gct tat aag cca ggc tca gaa tct gta cat acg	432
Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr	
130 135 140	
gtg gac aag cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt	480
Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val	
145 150 155 160	
tca act aaa caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt	528
Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly	
165 170 175	
gta caa gct tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta	576
Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu	
180 185 190	
aag tat gat tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa	624
Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys	
195 200 205	
act gat cag gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt	672
Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg	
210 215 220	
tta tct ctt cag cga gaa aag att atc gca agg gtg agt att gat aac	720
Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn	
225 230 235 240	
agg acc cgg gca tta gtt cag gca tta aga aga aca act gac cca aag	768
Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys	
245 250 255	
ctc tgc att act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt	816
Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe	
260 265 270	
cct gaa gga aaa gga gtg gct gtc aag gaa aga att att cca tat tta	864
Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu	
275 280 285	
tta cga ctg aga caa att aag gat gaa act ctt cag gct gca gtt aga	912
Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg	
290 295 300	

gaa att ttg gcc cta att ggc tat gtg gat cca gtg aaa ggg aga gga Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly 305 310 315 320	960
atc cga att ctc tca att gat ggt gga gga aca agg ggc gtg gtt gct Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala 325 330 335	1008
ctc cag acc cta cga aaa tta gtt gaa ctt act cag aag cca gtt cat Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His 340 345 350	1056
cag ctc ttt gat tac att tgt ggt gta agc aca ggt gcc ata tta gct Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala 355 360 365	1104
ttc atg ttg ggg ttg ttt cat atg ccc ttg gat gaa tgt gag gaa ctt Phe Met Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu 370 375 380	1152
tat cga aaa tta gga tca gat gta ttt tca caa aat gtc att gtt gga Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly 385 390 395 400	1200
aca gta aaa atg agt tgg agc cat gca ttt tat gac agt caa aca tgg Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp 405 410 415	1248
gaa aac att ctt aag gat agg atg gga tct gca ctg atg att gaa aca Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr 420 425 430	1296
gca aga aac ccc aca tgt cct aag gta gct gct gta agt acc ata gta Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val 435 440 445	1344
aat aga ggg ata aca ccc aaa gct ttt gtg ttc aga aac tat ggt cat Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His 450 455 460	1392
ttt cct gga atc aac tct cat tat ttg gga ggc tgt cag tat aaa atg Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met 465 470 475 480	1440
tgg cag gcc att aga gcc tca tct gct gct cca ggc tac ttt gca gaa Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu 485 490 495	1488
tat gca ttg gga aat gat ctt cat caa gat gga ggt ttg ctt ctg aat Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn 500 505 510	1536
aac cct tcg gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp 515 520 525	1584

gtg ccg tta gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt	1632
Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser	
530 535 540	
gat gtg aga aac acg gta aca tac aca agc ttg aaa act aaa ctt tct	1680
Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser	
545 550 555 560	
aat gtt atc aac agt gct aca gat aca gaa gaa gtc cat ata atg ctt	1728
Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu	
565 570 575	
gat ggc ctg tta cct cct gac acc tat ttt aga ttc aat cct gta atg	1776
Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met	
580 585 590	
tgt gaa aac ata cct cta gat gaa agt cga aat gaa aag ctg gat cag	1824
Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln	
595 600 605	
ctg cag ttg gaa ggg ttg aaa tac ata gaa aga aat gaa caa aaa atg	1872
Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met	
610 615 620	
aaa aaa gtt gca aaa ata tta agt caa gaa aaa aca act ctg cag aaa	1920
Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys	
625 630 635 640	
att aat gat tgg ata aaa tta aaa act gat atg tat gaa gga ctt cca	1968
Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro	
645 650 655	
ttc ttt tca aaa ttg tga	1986
Phe Phe Ser Lys Leu	
660	

<210> 20
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 gtaagtcgac aatgtctcaa caaaagg

27

<210> 21
 <211> 562
 <212> PRT
 <213> Homo sapiens

<400> 21
 Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu
 1 5 10 15

Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly
 20 25 30
 Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys
 35 40 45
 Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys
 50 55 60
 Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala
 65 70 75 80
 Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp
 85 90 95
 Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln
 100 105 110
 Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu
 115 120 125
 Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg
 130 135 140
 Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile
 145 150 155 160
 Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly
 165 170 175
 Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu
 180 185 190
 Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu
 195 200 205
 Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile
 210 215 220
 Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr
 225 230 235 240
 Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe
 245 250 255
 Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu
 260 265 270
 Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys
 275 280 285
 Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys
 290 295 300
 Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile
 305 310 315 320

[illegible]

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<210> 22
<211> 1689
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS

<222> (1) .. (1686)

<400> 22

atg tct caa caa aag gaa aat gaa cat ttc cgg gac aaa tca gaa ctt	48
Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu	
1 5 10 15	
gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca gat cct ggc	96
Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly	
20 25 30	
atc ctg gct tat aag cca ggc tca gaa tct gta cat acg gtg gac aag	144
Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys	
35 40 45	
cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt tca act aaa	192
Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys	
50 55 60	
caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt gta caa gct	240
Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala	
65 70 75 80	
tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta aag tat gat	288
Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp	
85 90 95	
tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa act gat cag	336
Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln	
100 105 110	
gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt tta tct ctt	384
Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu	
115 120 125	
cag cga gaa aag att atc gca agg gtg agt att gat aac agg acc cgg	432
Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg	
130 135 140	
gca tta gtt cag gca tta aga aga aca act gac cca aag ctc tgc att	480
Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile	
145 150 155 160	
act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt cct gaa gga	528
Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly	
165 170 175	
aaa gga gtg gct gtc aag gaa aga att att cca tat tta tta cga ctg	576
Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu	
180 185 190	
aga caa att aag gat gaa act ctt cag gct gca gtt aga gaa att ttg	624
Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu	
195 200 205	

gcc cta att ggc tat gtg gat cca gtg aaa ggg aga gga atc cga att Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile 210 215 220	672
ctc tca att gat ggt gga gga aca agg ggc gtg gtt gct ctc cag acc Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr 225 230 235 240	720
cta cga aaa tta gtt gaa ctt act cag aag cca gtt cat cag ctc ttt Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe 245 250 255	768
gat tac att tgt ggt gta agc aca ggt gcc ata tta gct ttc atg ttg Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu 260 265 270	816
ggg ttg ttt cat atg ccc ttg gat gaa tgt gag gaa ctt tat cga aaa Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys 275 280 285	864
tta gga tca gat gta ttt tca caa aat gtc att gtt gga aca gta aaa Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys 290 295 300	912
atg agt tgg agc cat gca ttt tat gac agt caa aca tgg gaa aac att Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile 305 310 315 320	960
ctt aag gat agg atg gga tct gca ctg atg att gaa aca gca aga aac Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn 325 330 335	1008
ccc aca tgt cct aag gta gct gct gta agt acc ata gta aat aga ggg Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly 340 345 350	1056
ata aca ccc aaa gct ttt gtg ttc aga aac tat ggt cat ttt cct gga Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly 355 360 365	1104
atc aac tct cat tat ttg gga ggc tgt cag tat aaa atg tgg cag gcc Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala 370 375 380	1152
att aga gcc tca tct gct gct cca ggc tac ttt gca gaa tat gca ttg Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu 385 390 395 400	1200
gga aat gat ctt cat caa gat gga ggt ttg ctt ctg aat aac cct tcg Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser 405 410 415	1248
gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat gtg ccg tta Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu 420 425 430	1296

gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt gat gtg aga	1344
Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg	
435 440 445	
aac acg gta aca tac aca agc ttg aaa act aaa ctt tct aat gtt atc	1392
Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile	
450 455 460	
aac agt gct aca gat aca gaa gaa gtc cat ata atg ctt gat ggc ctg	1440
Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu	
465 470 475 480	
tta cct cct gac acc tat ttt aga ttc aat cct gta atg tgt gaa aac	1488
Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn	
485 490 495	
ata cct cta gat gaa agt cga aat gaa aag ctg gat cag ctg cag ttg	1536
Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu	
500 505 510	
gaa ggg ttg aaa tac ata gaa aga aat gaa caa aaa atg aaa aaa gtt	1584
Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val	
515 520 525	
gca aaa ata tta agt caa gaa aaa aca act ctg cag aaa att aat gat	1632
Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp	
530 535 540	
tgg ata aaa tta aaa act gat atg tat gaa gga ctt cca ttc ttt tca	1680
Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser	
545 550 555 560	
aaa ttg tga	1689
Lys Leu	

<210> 23
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 gcatactcga gtcacaattt tgaaaagaat ggaagtcc 38

<210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 24
gtacatacgg tggacaagcc ta

22

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
cattcctctc cctttcactg gatccacata gcc

33

<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 26
Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln
1 5 10 15

<210> 27
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gaaaacctct ttgtagactg atgtggctta tcctccag

38

<210> 28
<211> 5
<212> PRT
<213> Homo sapiens

<400> 28
Ala Ser Cys Ser Val
1 5

<210> 29
<211> 302
<212> DNA
<213> Homo sapiens


```

<400> 29
tcagcagggt cagaacctat aatttcattc ggtatattct gtatgggtga agatgtacag 60
ccagcaaaag ctttttaatt cgggaaaaca cgattggact tgcactttca aaagattacc 120
gtggttgcac agaagagact gactgggtca gaggttagtt acaggctgga aaaccagttt 180
agatgaaact gaagagcaag gatgaaagcc tgaactagag cagtggaaat gcgaatgtgg 240
agcagaggaa cgattcaaga aattctgctg taaaactcat cagacttcat gactgattaa 300
ag                                                                 302

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<210> 30
<211> 118
<212> DNA
<213> Homo sapiens

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<400> 30
ttttgccttt ctagagtgtt atacagctgg aatcatactg gtaggtctat ggtccgaatg 60
tttgtgcttc tcaaaattca tgtggaaatc ataaccgcta aagtgatggt attaagag 118

```

```

<210> 31
<211> 92
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

```

```

<400> 31
tgtttgatgt ttttctgttt taaccagcca ctatccgata cttttcttaa aatttgggaa 60
cttggtctaa attgagctaa acgtgaaatc at                                                                 92

```

```

<210> 32
<211> 28
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

```

```

<400> 32
tcgacctgat ttcacgttta gctcaatt                                                                 28

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<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

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<400> 33
tcgactaagc caagttccca aattttaa 28

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 34
tcgacgaaaa gtatcggata gtggctgg 28

<210> 35
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 35
tcgacttaaa acagaaaaac atcaaaca 28

<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 36
ggactaaagt gcaaatcgag ttaaccgg 28

<210> 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 37
gattcggttc aagggtttaa aattccgg 28

<210> 38
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 38
 gcttttcata gcctatcacc gaccccg 28

<210> 39
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 39
 gaattttgtc tttttgtagt ttgtccgg 28

<210> 40
 <211> 353
 <212> PRT
 <213> Mus sp.

<400> 40
 Met Ser Ile Asn Leu Thr Leu Asp Ile Tyr Ile Tyr Phe Leu Asn Asn
 1 5 10 15
 Ala Arg Ser Leu Cys Gly Lys Gln Arg Ser Lys Gln Leu His Phe Val
 20 25 30
 Cys Ser Lys Gln Tyr Trp Arg Met Asn His Val Asn Val His Arg Glu
 35 40 45
 Phe His Thr Ser Lys Lys Ser Cys Lys Trp Asn Arg Ser Glu Ala His
 50 55 60
 Cys Ser Lys His Trp His Ser Pro Ser Asn His Gly Leu His Phe Gly
 65 70 75 80
 Ile Val Arg Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys Val Ser
 85 90 95
 Ile His Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser Lys Ala
 100 105 110
 Ile Phe Gly Ser Gln Asn Glu Met Val Thr Arg Leu Ala Gln Phe Lys
 115 120 125

Pro Ser Ser Arg Ile Leu Arg Lys Val Ser Asp Lys Gly Trp Leu Lys
 130 135 140
 Gln Lys Asn Val Lys Gln Ala Val Glu Ser Leu Lys Asn Tyr Ser Asp
 145 150 155 160
 Lys Ser Ala Gly Lys Asn Ser Leu Ala Glu Gln Lys Ser Tyr Phe Ala
 165 170 175
 Asp Lys Glu Glu Asp Ser Gly Lys His Ser Leu Phe His Tyr Thr Tyr
 180 185 190
 Gly Ile Thr Thr Arg Phe Gly Glu Ser Phe Ser Val Leu Ala Asn His
 195 200 205
 Ile Asn Ser Tyr Phe Lys Ser Lys Gly Lys Met Ser Gln Thr Lys Glu
 210 215 220
 Asp Lys Gln Leu Gln Asp Lys Pro Asp Leu Glu Glu Arg Lys Ser Ser
 225 230 235 240
 Ser Pro Gly Pro Asp Thr Val Ala Asp Arg Pro Asp Ser Glu Ser Pro
 245 250 255
 Leu Glu Val Lys Asp Lys Leu Ser Ser Pro Thr Gln Met Pro Glu Ala
 260 265 270
 His Pro Val Ser Ala Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro
 275 280 285
 Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val
 290 295 300
 Pro Lys Leu Lys Ser Asp Pro Lys Ser Pro Pro Glu Glu Gln Glu Val
 305 310 315 320
 Ser Ala Lys Thr Glu Gln Ala Val Asx Lys Asp Lys Lys Ala Glu Glu
 325 330 335
 Lys Lys Arg Val Leu Leu Gln Gln Glu Lys Ile Ile Ala Arg Val Ser
 340 345 350
 Ile

<210> 41
 <211> 353
 <212> PRT
 <213> Rattus sp.

<400> 41
 Met Ser Ile Asn Leu Ile Leu Asp Ile Tyr Ile Tyr Phe Leu Asn Asn
 1 5 10 15
 Ala Arg Ser Phe Cys Gly Lys Gln Arg Ser Lys Gln Leu Asn Phe Leu
 20 25 30

Cys Ser Lys Gln Tyr Trp Arg Met Asn His Val Asn Val His Arg Glu
 35 40 45
 Phe His Thr Ser Lys Lys Ser Cys Lys Trp Asn Arg Ser Glu Ala His
 50 55 60
 Cys Ser Lys His Trp His Ser Ser Ser Asn His Gly Val His Ile Gly
 65 70 75 80
 Ile Val Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys Val Ser
 85 90 95
 Ile His Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser Lys Ala
 100 105 110
 Ile Phe Gly Ser Gln Asn Glu Met Val Ser Arg Leu Ala Gln Phe Lys
 115 120 125
 Pro Ser Ser Arg Ile Phe Arg Lys Val Ser Asp Arg Gly Trp Leu Lys
 130 135 140
 His Lys Asn Val Lys Gln Ala Ile Glu Ser Leu Lys Asn Tyr Ser Asp
 145 150 155 160
 Lys Ser Ala Glu Lys Asn Ser Phe Ala Glu Gln Lys Ser Tyr Phe Ala
 165 170 175
 Asp Lys Glu Glu Gly Ser Asp Lys His Ser Leu Tyr His Tyr Ala Tyr
 180 185 190
 Arg Ile Thr Thr Arg Phe Gly Glu Ser Phe Tyr Phe Leu Ala Asn His
 195 200 205
 Ile Asn Ser Tyr Phe Lys Asn Lys Glu Lys Met Ser Gln Thr Lys Glu
 210 215 220
 Asp Arg Gln Leu Gln Asp Lys Pro Cys Leu Glu Glu Ser Lys Ser Ile
 225 230 235 240
 Ser Pro Ser Pro Asp Ile Leu Thr Asp Arg Pro Asp Ser Gly Pro Pro
 245 250 255
 Leu Asn Val Glu Asp Lys Leu Ser Ser Ser Thr Gln Leu Pro Glu Ala
 260 265 270
 Leu Pro Val Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro
 275 280 285
 Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val
 290 295 300
 Pro Lys Leu Lys Ser Asp Pro Lys Ser Gln Pro Glu Glu Glu Glu Glu
 305 310 315 320
 Pro Ser Lys Thr Asp Glu Pro Ile Cys Lys Asp Lys Lys Ala Glu Glu
 325 330 335

Lys Lys Arg Val Leu Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser
 340 345 350

Ile

<210> 42

<211> 359

<212> PRT

<213> Homo sapiens

<400> 42

Met Ser Ile Asn Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn
 1 5 10 15

Ala Arg Ser Val Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
 20 25 30

Phe Ser Pro Lys His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg
 35 40 45

Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala
 50 55 60

His Ser Cys Ser Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His
 65 70 75 80

Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys
 85 90 95

Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser
 100 105 110

Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln
 115 120 125

Phe Lys Pro Ser Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp
 130 135 140

Leu Lys Gln Lys Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr
 145 150 155 160

Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His
 165 170 175

Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr
 180 185 190

Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser
 195 200 205

Asn His Ile Asn Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln
 210 215 220

Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys
 225 230 235 240
 Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr
 245 250 255
 Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro
 260 265 270
 Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala
 275 280 285
 Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly
 290 295 300
 Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln
 305 310 315 320
 Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys
 325 330 335
 Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys
 340 345 350
 Ile Ile Ala Arg Val Ser Ile
 355

<210> 43
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(12)

<400> 43
 cag cga gaa aag gcaagtt
 Gln Arg Glu Lys
 1

19

<210> 44
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 44
 Gln Arg Glu Lys
 1

<210> 45
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(18)

<400> 45
 att atc gca agg gtg agt
 Ile Ile Ala Arg Val Ser
 1 5

18

<210> 46
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 46
 Ile Ile Ala Arg Val Ser
 1 5

<210> 47
 <211> 26
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(20)

<400> 47
 gaa aag gca agt tgt tca gt gtgctt
 Glu Lys Ala Ser Cys Ser Val
 1 5

26

<210> 48
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 48
 Glu Lys Ala Ser Cys Ser Val
 1 5

<210> 49
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Illustrative
 conserved lipase motif

<220>
 <221> MOD_RES

<222> (2)
 <223> Variable amino acid

<400> 49
 Gly Xaa Ser Gly Ser
 1 5

<210> 50
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Illustrative
 conserved motif

<220>
 <221> MOD_RES
 <222> (2)
 <223> Variable amino acid

<400> 50
 Gly Xaa Ser Thr Gly
 1 5

<210> 51
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 51
 Ile Ile Ala Arg
 1

<210> 52
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 52
 Ile Cys Gly Val Ser Thr Gly
 1 5

<210> 53
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 53
 Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly
 1 5 10

<210> 54
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 6-His tag

<400> 54
 His His His His His His
 1 5

<210> 55
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 55
 aaaagtcgac atgaagccat caaatctc 28

<210> 56
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 56
 aagagtcgac atgaggtaaa cgcagtc 27

<210> 57
 <211> 315
 <212> DNA
 <213> Homo sapiens

<400> 57
 atgtctatta atctgactgt agatatatat atttacctcc ttagtaatgc aagaagtgtt 60
 tgtgggaagc agagaagcaa gcaactgtat ttcttggtct cacctaagca ttactggagg 120
 ataagccaca tcagtctaca aagaggtttt catacaaaca taataagatg taaatggacc 180
 aaaagtgaag cacattcttg cagtaagcac tggtactctc caagcaacca tggtttacat 240
 attgggattt tgaaacttag cacttctgct cccaagggac ttacaaaagt gaacatttgt 300
 atgtcccgtg ttaaa 315

<210> 58
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 58

Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser Ser Gln Ile Leu Arg
 1 5 10 15

Lys Val Ser

<210> 59

<211> 45

<212> DNA

<213> Homo sapiens

<400> 59

tattaatctg actgtagata tatatatatta cctccttagt aatgc 45

<210> 60

<211> 6

<212> DNA

<213> Homo sapiens

<400> 60

caagtg 6

<210> 61

<211> 6

<212> DNA

<213> Homo sapiens

<400> 61

caggtg 6

<210> 62

<211> 6

<212> DNA

<213> Homo sapiens

<400> 62

caggtg 6

<210> 63

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 63

gttgaagctt gtgtctatta atctgactgt a 31

<210> 64
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 64
 tagaccatgg tggcttatcc tccagtaatg c 31

<210> 65
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 65
 gtgtaagctt gaagcagaga agcaagcaac tg 32

<210> 66
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 66
 actgccatgg tggccttcac ttttggtcca tttac 35

<210> 67
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 67
 tggaaagctt gccacatcag tctacaaag 29

<210> 68
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 68
 tgctccatgg tggcatccca atatgtaaac ca 32

<210> 69
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 69
 gaaccaagct tgaagcacat tcttgagta agca 34

<210> 70
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 70
 caaaacatgt tggctacggg acatacaaat gttca 35

<210> 71
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 71
 gttgaagctt tttgaaactt agcacttctg c 31

<210> 72
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 72
 attccatggg ggctgaaatc atttcatttt gattgcc 37

<210> 73
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

 <400> 73
 tcaaaaagctt atgatttcac gtttagctc 29

 <210> 74
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 74
 ctttccatgg tggctgtcac tatatttttt ca 32

 <210> 75
 <211> 18
 <212> DNA
 <213> Homo sapiens

 <400> 75
 gattaaaggt atggtggt 18

 <210> 76
 <211> 19
 <212> DNA
 <213> Homo sapiens

 <400> 76
 acctccttag taatgcaag 19

 <210> 77
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <400> 77
 gcgtcacttc cgctgggggc gg 22

 <210> 78
 <211> 11
 <212> DNA
 <213> Homo sapiens

 <400> 78
 gccagtgttt g 11

 <210> 79
 <211> 13

<212> DNA
 <213> Homo sapiens

<400> 79
 ttttaagtta tgt 13

<210> 80
 <211> 13
 <212> DNA
 <213> Homo sapiens

<400> 80
 aacatttgta tgt 13

<210> 81
 <211> 13
 <212> DNA
 <213> Homo sapiens

<400> 81
 caaaatgaaa tga 13

<210> 82
 <211> 13
 <212> DNA
 <213> Homo sapiens

<400> 82
 aaggaaaaaa tgt 13

<210> 83
 <211> 13
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 83
 gccgccrcca tgg 13

<210> 84
 <211> 270
 <212> DNA
 <213> Homo sapiens

<400> 84
 attataatac tgtgcagcaa gggcaataag agaagtgagc acaggtggaa ggaatgattc 60
 attctatgag tagtgaggta agattttcct ggctgaagga caaacaaatc tttaggagga 120
 caaggtggaa ggggagctaa gccaacagca tgaccaaggc actaagtatg aaaaggaaca 180
 agagtatctg gggaagtaca ggtgtggctg gaggatagag agtgagaggc aagtggtgaa 240

agtaaaggct ggaaggctcag cagggtcaga 270

<210> 85
 <211> 11
 <212> DNA
 <213> Homo sapiens

<400> 85
 ggacaggtgg g 11

<210> 86
 <211> 11
 <212> DNA
 <213> Homo sapiens

<400> 86
 cacaggtggt g 11

<210> 87
 <211> 12
 <212> DNA
 <213> Homo sapiens

<400> 87
 cgacaggtgg tg 12

<210> 88
 <211> 64
 <212> DNA
 <213> Mus sp.

<400> 88
 gcgtcacttc cgctgggggc ggggcgtagc ggtgggtggt gctgggcacg ccagtgtttg 60
 ggg 64

<210> 89
 <211> 63
 <212> DNA
 <213> Rattus sp.

<400> 89
 gcgtcacttc cgctgggggc ggggcgtagc ggaggggtgag gctgtagcgc cagtgtttg 60
 ggt 63

<210> 90
 <211> 76
 <212> DNA
 <213> Homo sapiens

<400> 90
 gcgtcacttc cgctgggggc ggagcggggc ggggctgagt ggggtggcgac ctagctgctg 60

cgccagtgtt tgtgtt 76

<210> 91
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 91
 gcatcccggt aagtagcc 18

<210> 92
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 92
 acctccttag taatgcaag 19

<210> 93
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 93
 gtggccgggt ggtccacctc gg 22

<210> 94
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 94
 ttgatagtta tctattacag tcttcttaga ttgaaacaa 39

<210> 95
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 95
 Leu Arg Lys Val Ser
 1 5

<210> 96
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 96
 Gly Gly Gly Thr Arg Gly
 1 5

<210> 97
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 97
 Gly Val Ser Thr Gly
 1 5

<210> 98
 <211> 11
 <212> DNA
 <213> Homo sapiens

<400> 98
 tctcacctaa g

11

<210> 99
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 99
 Asn His Gly Leu Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala
 1 5 10

<210> 100
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 100
 Lys Val Asn Ile Cys Met
 1 5

<210> 101
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 101
 Asn Gln Asn Glu Met Ile
 1 5

<210> 102
<211> 4
<212> PRT
<213> Homo sapiens

<400> 102
Ile Ser Arg Leu
1

<210> 103
<211> 4
<212> PRT
<213> Homo sapiens

<400> 103
Ile Gly Lys Arg
1

<210> 104
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 104
tattaatctg actgtagata tatatattta cctccttagt aatgc